

OF6 Comparative Quantitative Analysis of Mouse Adipose and Liver Tissue using LC-MALDI TOF/TOF and LTQ Orbitrap XL

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High end trans-technology wide quantitative analysis of obese mouse tissue samples.

Recent advances in the quantification of complex protein samples are based on the availability of faster and more sensitive mass spectrometers and on the improvement of quantitative sample labelling protocols. We applied such technologies for the identification and quantification of adipose and liver tissue from obese mice [1] using an LTQ OrbitrapXL and LC-MALDI-TOFTOF analyser. It was previously reported that in the OrbitrapXL peptide ions can be efficiently fragmented by high-accuracy and full-mass-range MSMS via higher-energy C-trap dissociation (HCD) [2].

Using HCD fragmentation we produce robust precursor ion fragmentation, and routinely scan product ions down to m/z 50 enabling for iTRAQ™ experiments. On the other hand ion trap CID fragmentation usually produces best quality spectra for peptide identification. We have developed a method where spectral merging of CID and HCD of two consecutive scans from the same precursor ion, increases the number of identified peptides in average by 30% thus significantly improves protein quantitation in complex mixtures.

We can conclude that the sensitivity of the quantitative workflow on the OrbitrapXL is at least 3x higher than on the LC-MALDI-TOFTOF. To further evaluate the two applied technologies we also show the ratio correlation of samples analysed on the two platforms.

[1] A. Chadt, H. Al-Hasani, Nature Genetics 40, 1354 – 1359, 2008

[2] Mann et al. Nature Methods 4, 709 – 712, 2007